Figure S1: Feasible γ (gamma) parameter ranges for flexFBA of the iMC1010 *E. coli* metabolic network, including those frustrated by many knockdowns. For each 'number of knockdowns' N, a randomly selected N of the f_i fluxes were constrained with an upper bound of 10% the wild-type value. Random selection was repeated for 10 random samples at each N. Networks were then simulated at many γ values, and visualized as follows: a green line extends from the first value of γ at which all unconstrained $f_i = f_{\text{atp}}$, to the highest; a grey line extends over the γ range for which all $f_i = \bar{f}$ of the biomass reaction; black indicates all $f_i = 0$ and extends across γ greater than those shown. Regions without markings (whitespace at low γ) are characterized by nonzero f_{atp}, but where some subset of unconstrained f_i are 0. Selection and simulation procedure was carried out for three growth rates μ, meaning three different f_{atp} values, set via change in the glucose and oxygen uptake rates flux bounds which produce: (A) $\mu_{\text{low}} = 0.3$/h which is about half the glucose growth rate; (B) $\mu_{\text{mid}} = 0.69$/h corresponding to aerobic growth on glucose minimal media; (C) $\mu_{\text{high}} = 1.42$/h which is about twice the glucose growth rate.